

FINDPATTERNS: on geneseqp: allowing 0 mismatches	
1 (P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	May
<i>wa</i> <i>accession #</i> <i>to match db</i> <i>to o. filter</i>	
1 AAW32305 ck: 992 len: 542 i Aaw32305 Arabidopsis thaliana inorganic phd	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L) - pattern matched	
130: GVMAT (L)XFX(R)(F)WXX(F) - pattern matched	
LCFFRFWLGCF	GIGGD
1 AAW32302 ck: 605 len: 534 i Aaw32302 Arabidopsis thaliana inorganic phd	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
130: GVMAT (L)XFX(R)(F)WXX(F)	
LCFFRFWLGCF	GIGGD
1 AAW32303 ck: 4821 len: 521 i Aaw32303 Arabidopsis thaliana inorganic phd	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
130: GVMAT (L)XFX(R)(F)WXX(F)	
LCFFRFWLGCF	GIGGD
1 AAW32304 ck: 8027 len: 524 i Aaw32304 Arabidopsis thaliana inorganic phd	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
130: GVMAT (L)XFX(R)(F)WXX(F)	
LCFFRFWLGCF	GIGGD
1 AAW32301 ck: 8746 len: 524 i Aaw32301 Arabidopsis thaliana inorganic phd	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
130: GVMAT (L)XFX(R)(F)WXX(F)	
LCFFRFWLGCF	GIGGD
1 AAW30486 ck: 8893 len: 135 i Aaw30486 Flea saliva protein fispn6-1	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
108: HFDAM (P)XFX(R)(F)WXX(O)	
PGFSRFWMNPO	QCPAY
1 AAW36137 ck: 605 len: 534 i Aaw36137 A. thaliana inorganic phosphate tr	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
130: AVMAT (L)XFX(R)(F)WXX(F)	
LCFFRFWLGCF	GIGGD
1 AAW82377 ck: 8893 len: 135 i Aaw82377 Flea saliva protein fispn6-135. 4/	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
108: HFDAM (P)XFX(R)(F)WXX(O)	
PGFSRFWMNPO	QCPAY
1 AAW82382 ck: 6654 len: 375 i Aaw82382 Flea saliva protein fispn6-375. 4/	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
134: HFDAM (P)XFX(R)(F)WXX(O)	
PGFSRFWMNPO	QCPAY
1 AAW82384 ck: 2624 len: 356 i Aaw82384 Flea saliva protein fispn6-356. 4/	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
115: HFDAM (P)XFX(R)(F)WXX(O)	
PGFSRFWMNPO	QCPAY
<hr/>	
1 AAW82385 ck: 309 len: 355 i Aaw82385 Flea saliva protein fispn6-357.	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
114: HFDAM (P)XFX(R)(F)WXX(O)	
PGFSRFWMNPO	QCPAY
1 AAW82322 ck: 4400 len: 19 i Aaw82322 p53 homologue TIP 12/1 peptide.	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
6: PPLSM (P)XFX(D)(Y)WXX(L)	
PRFMDYWEGL	NENG
1 AAW82320 ck: 4400 len: 19 i Aaw82320 p53 homologue TIP 12/1 peptide.	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
6: PPLSM (P)XFX(D)(Y)WXX(L)	
PRFMDYWEGL	NENG
1 AAW58852 ck: 5772 len: 130 i Aaw58852 Human O289_1 secreted protein.	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
6: PPLSM (P)XFX(D)(Y)WXX(L)	
PRFMDYWEGL	NENG
119: VISHL CHFSSTFICGL	PA
1 AAW56025 ck: 9188 len: 316 i Aaw56025 Phosphate starvation-induced pr	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
31: SVMAT (L)XFX(R)(F)WXX(F)	
LCFFRFWLGCF	GIGGD
1 AAW37220 ck: 5978 len: 12 i Aaw37220 KDM2 binding peptide unique pha	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
2: M (P)XFX(D)(Y)WXX(L)	
PREMDYWEGL	N
1 AAW37224 ck: 9428 len: 15 i Aaw37224 KDM2 binding peptide unique pha	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
5: PRPA (L)XFX(D)(Y)WXX(L)	
LVFADYWEGL	Y
1 AAW37221 ck: 6151 len: 12 i Aaw37221 KDM2 binding peptide unique pha	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
2: V (O)XFX(D)(Y)WXX(O)	
QNFIDYWTQO	F
1 AAW37222 ck: 5993 len: 12 i Aaw37222 KDM2 binding peptide unique pha	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
3: TG (P)XFX(R)(F)WXX(F)	
PATFHYVATF	
1 AAW37223 ck: 9093 len: 15 i Aaw37223 KDM2 binding peptide unique pha	1
(P,L,E,C,Q)XFX(R,H,E,C,S,D)(H,F,Y)WXX(F,Q,L)	
5: IDRA (P)XFX(D)(H)WXX(L)	
PTFRDHWFAL	V
1 AAW37225 ck: 8833 len: 15 i Aaw37225 KDM2 binding peptide unique pha	1

=> fil reg; d que 13

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STRUCTURE FILE UPDATES: 28 MAY 2002 HIGHEST RN 422506-41-0
DICTIONARY FILE UPDATES: 28 MAY 2002 HIGHEST RN 422506-41-0

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

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Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
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Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

L2 259 SEA FILE=REGISTRY ABB=ON [PLECQ].F.[RHECSD][HFY]W..[FQL]/SQSP

L3 2 SEA FILE=REGISTRY ABB=ON L2 AND SQL<11

sequence length less than 11

=> d rn cn kwic nte 13 1-2; fil capl; d que 14

L3 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2002 ACS

RN 393113-23=0° REGISTRY *use Registry # to match sequence to citation*

CN L-Leucine, L-prolyl-L-arginyl-L-phenylalanyl-L-methionyl-L-.alpha.-
aspartyl-L-tyrosyl-L-tryptophyl-L-.alpha.-glutamylglycyl- (9CI) (CA INDEX
NAME)

*sequence
length* SQL 10

SEQ 1 PRFMDYWEGL

HITS AT: 1-10

L3 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2002 ACS

RN 267004-47-7 REGISTRY

CN Peptide, (Pro-Xaa-Phe-Xaa-Asp-Tyr-Trp-Xaa-Xaa-Leu) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 109: PN: W00024782 SEQID: 142 claimed protein

CN 727: PN: W00183525 TABLE: 13 claimed protein

SQL 10

SEQ 1 PXFXDYWXXL

HITS AT: 1-10

NTE

type	location	description
uncommon	Aaa-2	-
uncommon	Aaa-4	-
uncommon	Aaa-8	-
uncommon	Aaa-9	-

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L2 259 SEA FILE=REGISTRY ABB=ON [PLECQ].F.[RHECSD][HFY]W..[FQL]/SQSP
L3 2 SEA FILE=REGISTRY ABB=ON L2 AND SQL<11
L4 3 SEA FILE=CAPLUS ABB=ON L3

=> d ibib ab hitrn l4 1-3

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:829830 CAPLUS
DOCUMENT NUMBER: 136:128583
TITLE: QSAR: hydropathic analysis of inhibitors of the

AUTHOR(S): Galatin, Peter S.; Abraham, Donald J.
CORPORATE SOURCE: Department of Medicinal Chemistry and Institute for
Structural Biology and Drug Discovery, Virginia
Commonwealth University, Richmond, VA, 23298, USA
SOURCE: Proteins: Structure, Function, and Genetics (2001),
45(3), 169-175
CODEN: PSFGEY; ISSN: 0887-3585
PUBLISHER: Wiley-Liss, Inc.

DOCUMENT TYPE: Journal
LANGUAGE: English

AB To date, a no. of p53-derived peptides have been evaluated in vitro for their ability to inhibit the carcinogenic p53-mdm2 interaction. Design of second-generation nonpeptidic compds. requires the redn. of large peptide structures down to small mols. maintaining the proper spatial arrangement of key functional groups. Mol. modeling software exists that can predict and rank intermol. interactions from the p53-mdm2 complex crystal structure. Such analyses can yield a pharmacophore model suitable as a search query for a 3D chem. database to generate new lead compds. As preliminary validation of this methodol., the Hydropathic INTERactions (HINT) program has been used to generate noncovalent interaction measurements between reported peptide inhibitors and mdm2. Quant. structure-activity relationships were developed expressing peptide